

Database : A\_Geneseq\_16Dec04:\*

- 1: geneseqp1980s:\*
- 2: geneseqp1990s:\*
- 3: geneseqp2000s:\*
- 4: geneseqp2001s:\*
- 5: geneseqp2002s:\*
- 6: geneseqp2003as:\*
- 7: geneseqp2003bs:\*
- 8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2619	100.0	514	7	ADG63312	Adg63312 Human IMP
2	2609	99.6	514	7	ADG63349	Adg63349 Human IMP
3	2605	99.5	514	2	AAR05432	Aar05432 Human IMP
4	2605	99.5	514	5	AAE18189	Aae18189 Human wil
5	2605	99.5	514	7	ADG63310	Adg63310 Human wil
6	2605	99.5	514	7	ADJ68634	Adj68634 Human hea
7	2605	99.5	514	8	ADO19228	Ado19228 Human PRO
8	2605	99.5	529	8	ADR66377	Adr66377 Human pro
9	2605	99.5	529	8	ADR66719	Adr66719 Human pro
10	2601	99.3	514	7	ADG63316	Adg63316 Human IMP
11	2601	99.3	514	7	ADG63314	Adg63314 Human IMP
12	2597	99.2	514	7	ADG63318	Adg63318 Human IMP
13	2595	99.1	514	5	AAU10695	Aau10695 Reference
14	2595	99.1	514	5	AAE18186	Aae18186 Human wil
15	2595	99.1	514	8	ADS88152	Ads88152 Human pro
16	2590	98.9	514	7	ADG63320	Adg63320 Human IMP
17	2569	98.1	514	7	ADG63340	Adg63340 Mouse IMP
18	2559	97.7	514	2	AAR05431	Aar05431 Chinese h
19	2555	97.6	514	7	ADG63338	Adg63338 Mouse wil
20	2234	85.3	514	5	AAE18188	Aae18188 Human wil
21	2234	85.3	514	5	ADI17228	Adi17228 Human NOV
22	2234	85.3	563	6	ADA54125	Ada54125 Human pro
23	2229	85.1	514	5	AAE18257	Aae18257 Human typ



Db	121	LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVLGIISSRDIDFLKEEEHDCFLEEIMT	180
Qy	181	KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA	240
Db	181	KREDLVVAPRSITLKEANEILQRSKKGKLPIVNEDDELVAIIARTDLKKNRDYPLASKDA	240
Qy	241	KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI	300
Db	241	KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI	300
Qy	301	GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIIQEV LACGRPQATAVYKVY EYARRFGVP	360
Db	301	GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEV LACGRPQATAVYKVSEYARRFGVP	360
Qy	361	VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Db	361	VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Qy	421	DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR	480
Db	421	DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR	480
Qy	481	AMMYSGELKF EKRTSSAQVEGGVHSLHSYEKRLF	514
Db	481	AMMYSGELKF EKRTSSAQVEGGVHSLHSYEKRLF	514

Database :           Published\_Applications\_AA:\*

- 1:   /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2:   /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3:   /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4:   /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5:   /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6:   /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7:   /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8:   /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9:   /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10:  /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11:  /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12:  /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13:  /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14:  /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15:  /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16:  /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17:  /cgn2\_6/ptodata/2/pubpaa/US10E\_PUBCOMB.pep:\*
- 18:  /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 19:  /cgn2\_6/ptodata/2/pubpaa/US11A\_PUBCOMB.pep:\*
- 20:  /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 21:  /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 22:  /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2619	100.0	514	10	US-09-846-637A-4		Sequence 4, Appli
2	2605	99.5	514	9	US-09-853-918-63		Sequence 63, Appl
3	2605	99.5	514	10	US-09-846-637A-2		Sequence 2, Appli
4	2605	99.5	514	16	US-10-408-765A-440		Sequence 440, App
5	2601	99.3	514	10	US-09-846-637A-6		Sequence 6, Appli
6	2601	99.3	514	10	US-09-846-637A-8		Sequence 8, Appli
7	2597	99.2	514	10	US-09-846-637A-10		Sequence 10, Appl
8	2595	99.1	514	9	US-09-853-918-49		Sequence 49, Appl
9	2590	98.9	514	10	US-09-846-637A-12		Sequence 12, Appl

Database :            Issued\_Patents\_AA:\*

1:    /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2:    /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3:    /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*

4:    /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*

5:    /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*

6:    /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	2605	99.5	514	3	US-08-925-230-7	Sequence 7, Appli	
2	2605	99.5	514	4	US-09-712-372-7	Sequence 7, Appli	
3	2595	99.1	514	4	US-09-538-092-913	Sequence 913, App	
4	2595	99.1	607	4	US-09-949-016-11614	Sequence 11614, A	
5	2559	97.7	514	3	US-08-925-230-8	Sequence 8, Appli	
6	2559	97.7	514	4	US-09-712-372-8	Sequence 8, Appli	
7	2222	84.8	514	4	US-09-538-092-973	Sequence 973, App	
8	1607.5	61.4	523	4	US-09-538-092-584	Sequence 584, App	
9	1210.5	46.2	371	3	US-09-212-247C-9	Sequence 9, Appli	
10	906	34.6	510	4	US-09-134-000C-5141	Sequence 5141, Ap	
11	885	33.8	495	4	US-09-107-532A-4081	Sequence 4081, Ap	
12	865	33.0	488	4	US-09-710-279-2308	Sequence 2308, Ap	
13	865	33.0	494	3	US-09-134-001C-5024	Sequence 5024, Ap	
14	862.5	32.9	558	4	US-09-252-991A-18187	Sequence 18187, A	
15	859.5	32.8	497	4	US-09-328-352-6297	Sequence 6297, Ap	
16	819	31.3	510	4	US-09-489-039A-11778	Sequence 11778, A	
17	816	31.2	487	4	US-09-809-665A-169	Sequence 169, App	
18	811	31.0	487	4	US-09-809-665A-24	Sequence 24, Appl	
19	807.5	30.8	492	4	US-09-583-110-4390	Sequence 4390, Ap	



Db	121	 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVLVGIISSRDIDFLKEEEHDCFLEEIMT	180
Qy	181	KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA	240
Db	181	 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA	240
Qy	241	KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI	300
Db	241	 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI	300
Qy	301	GGNVVTAAQAKNLIDAGVDALRVGMGSGSICI IQEVLACGRPQATAVYKVVEYARRFGVP	360
Db	301	 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVP	360
Qy	361	VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Db	361	 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM	420
Qy	421	DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR	480
Db	421	 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR	480
Qy	481	AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF	514
Db	481	 AMMYSGELKFEKRTSSAQVEGGVHSLHSYEKRLF	514

Database : PIR\_79:\*  
 1: pirl:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

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# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2595	99.1	514	1	A31997	IMP dehydrogenase
2	2559	97.7	514	1	B31997	IMP dehydrogenase
3	2555	97.6	514	1	JT0565	IMP dehydrogenase
4	2222	84.8	514	1	A35566	IMP dehydrogenase
5	1764.5	67.4	537	1	S41064	IMP dehydrogenase
6	1635.5	62.4	537	1	S59508	IMP dehydrogenase
7	1610.5	61.5	524	1	S50890	IMP dehydrogenase
8	1607.5	61.4	523	1	S59402	IMP dehydrogenase
9	1589.5	60.7	523	1	S48997	IMP dehydrogenase
10	1473.5	56.3	524	1	T40127	IMP dehydrogenase
11	1385.5	52.9	512	1	A55407	IMP dehydrogenase
12	1363.5	52.1	514	1	A38668	IMP dehydrogenase
13	1324.5	50.6	499	1	T32709	IMP dehydrogenase
14	1155	44.1	502	2	F86298	IMP dehydrogenase
15	1106.5	42.2	503	1	JC4999	IMP dehydrogenase
16	1043.5	39.8	403	2	S53477	IMP dehydrogenase
17	966.5	36.9	485	2	G81308	IMP dehydrogenase
18	958	36.6	485	2	D97232	IMP dehydrogenase



RESULT 1

A31997

IMP dehydrogenase (EC 1.1.1.205) II - human

N;Alternate names: inosine 5'-monophosphate dehydrogenase (IMPDH) type II

C;Species: Homo sapiens (man)

C;Date: 21-May-1990 #sequence\_revision 22-May-1998 #text\_change 09-Jul-2004

C;Accession: I52303; I54184; A92676; B35566; A31997; A94550

R;Glesne, D.A.; Huberman, E.

Biochem. Biophys. Res. Commun. 205, 537-544, 1994

A;Title: Cloning and sequence of the human type II IMP dehydrogenase gene.

A;Reference number: I52303; MUID:95091778; PMID:7999076

A;Accession: I52303

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-514 <GLE1>

A;Cross-references: UNIPROT:P12268; GB:L33842; NID:g602457; PIDN:AAA67054.1; PID:g602458

R;Glesne, D.A.; Collart, F.R.; Varkony, T.; Drabkin, H.; Huberman, E.

Genomics 16, 274-277, 1993

A;Title: Chromosomal localization and structure of the human type II IMP dehydrogenase gene.

A;Reference number: I54184; MUID:93252398; PMID:8098009

A;Accession: I54184

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 461-514 <GLE2>

A;Cross-references: GB:L08114; NID:g292239; PIDN:AAA36113.1; PID:g292240

R;Collart, F.R.; Huberman, E.

J. Biol. Chem. 263, 15769-15772, 1988

A;Title: Cloning and sequence analysis of the human and Chinese hamster inosine-5'-monophosphate dehydrogenase cDNAs.

A;Reference number: A92676; MUID:89008491; PMID:2902093

A;Accession: A92676

A;Molecule type: mRNA

A;Residues: 1-189,'RS',192-514 <COL>

A;Cross-references: GB:J04208; NID:g186391; PIDN:AAA36112.1; PID:g307066

A;Note: submitted to the Protein Sequence Database, November 1989

R;Natsumeda, Y.; Ohno, S.; Kawasaki, H.; Konno, Y.; Weber, G.; Suzuki, K.

J. Biol. Chem. 265, 5292-5295, 1990

A;Title: Two distinct cDNAs for human IMP dehydrogenase.

A;Reference number: A35566; MUID:90203022; PMID:1969416

A;Accession: B35566

A;Status: nucleic acid sequence not shown; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-514 <NAT>

C;Comment: mRNA for IMP dehydrogenase I (see PIR:A35566) predominated in normal leukocytes, whereas that for IMP dehydrogenase II predominated in ovarian tumor cells.

C;Genetics:

A;Gene: GDB:IMPDH2

A;Cross-references: GDB:128086; OMIM:146691

A;Map position: 3p24.2-3p21.2

A;Introns: 33/2; 49/3; 83/3; 108/3; 177/3; 207/1; 274/1; 304/1; 336/1; 432/2; 480/2; 508/2

C;Function:

A;Description: catalyzes the oxidation of inosine 5'-phosphate by NAD and one molecule of water to xanthosine 5'-phosphate

A;Pathway: purine nucleotide biosynthesis

C;Superfamily: inosine-5'-monophosphate dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal homology; IMP dehydrogenase catalytic homology

C;Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

F;30-96/Domain: IMP dehydrogenase amino-terminal homology <IDHN>

F;117-168/Domain: CBS homology <CBS1>

F;184-232/Domain: CBS homology <CBS2>

F;233-476/Domain: IMP dehydrogenase catalytic homology <IDHC>

F;331/Active site: Cys #status predicted

Query Match 99.1%; Score 2595; DB 1; Length 514;  
Best Local Similarity 99.2%; Pred. No. 8.7e-159;  
Matches 510; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy      1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MADYLISGGTSYVPDDGLTAQQLFNCGDGLTYNDFLILPGYIDFTADQVDLTSALTKKIT 60

Qy     61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LKTPLVSSPMDTVTEAGMAIAMALTGGIGFIHHNCTPEFQANEVRKVKKYEQGFITDPVV 120

Qy    121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVLVGIISSRDIDFLKEEEHDCFLEEIMT 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 LSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRVLVGIISSRDIDFLKEEEHDCFLEEIMT 180

Qy    181 KREDLVVAPRSITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240
        ||||||||  ||||||||||||||||||||||||||||||||||||||||||||
Db    181 KREDLVVAPAGITLKEANEILQRSKKGKLPVNEDELVAIIARTDLKKNRDYPLASKDA 240

Qy    241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVLDSSQGNSIFQINMIKYIKDKYPNLQVI 300

Qy    301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICIIQEVLACGRPQATAVYKVYEYARRFGVP 360
        ||||||||||||||||||||||||||||||||||||  ||||||||||||||||
Db    301 GGNVVTAAQAKNLIDAGVDALRVGMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVP 360

Qy    361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 VIADGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKYRGMGSLDAM 420

Qy    421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 DKHLSSQNRYFSEADKIKVAQGVSGAVQDKGSIHKFVPYLIAGIQHSCQDIGAKSLTQVR 480

Qy    481 AMMYSGELKF EKRTSSAQVEGGVHSLHSYEKRLF 514
        ||||||||||||||||||||||||||||||||
Db    481 AMMYSGELKF EKRTSSAQVEGGVHSLHSYEKRLF 514
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Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
1	2595	99.1	514	1	IMD2_HUMAN	P12268 homo sapien	
2	2561	97.8	514	1	IMD2_MOUSE	P24547 mus musculu	
3	2559	97.7	514	1	IMD2_CRIGR	P12269 cricetulus	
4	2547	97.3	514	2	Q6P9U9	Q6p9u9 rattus norv	
5	2422	92.5	514	2	Q66JD5	Q66jd5 xenopus tro	
6	2411	92.1	514	2	Q7ZYP7	Q7zyp7 xenopus lae	
7	2404	91.8	514	2	Q7ZXT8	Q7zxt8 xenopus lae	
8	2395	91.4	514	2	Q7ZYW9	Q7zyw9 brachydanio	
9	2256	86.1	514	2	Q7ZWN1	Q7zwn1 xenopus lae	
10	2253	86.0	544	2	Q6GMG5	Q6gmg5 brachydanio	
11	2234	85.3	514	1	IMD1_HUMAN	P20839 homo sapien	
12	2222	84.8	514	2	Q7TSG7	Q7tsg7 mus musculu	
13	2203	84.1	514	1	IMD1_MOUSE	P50096 mus musculu	
14	2093.5	79.9	530	2	Q6ZNB1	Q6znb1 homo sapien	
15	1830.5	69.9	559	2	Q7QHD0	Q7qhd0 anopheles g	
16	1764.5	67.4	537	1	IMDH_DROME	Q07152 drosophila	
17	1614.5	61.6	522	2	Q756Z6	Q756z6 ashbya goss	
18	1610.5	61.5	524	1	IMD4_YEAST	P50094 saccharomyc	
19	1608.5	61.4	526	2	Q6C897	Q6c897 yarrowia li	
20	1607.5	61.4	523	1	IMD3_YEAST	P50095 saccharomyc	
21	1605.5	61.3	521	1	IMH3_CANAL	O00086 candida alb	
22	1597.5	61.0	521	2	Q9P8J2	Q9p8j2 candida alb	